

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 07:25:40 ; Search time 727.75 Seconds
(without alignments)
2735.846 Million cell updates/sec

Title: US-09-227-881-1

Perfect score: 5300

Sequence: 1 attcttgctcagtttaccctc.....caggcactctcagcacagc 5300

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

N_Geneseq_36:*

- 1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
- 2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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- 20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
- 21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5299	100.0	5300	19	Human TIGR promote
2	5298.4	100.0	5300	19	Human TIGR promote
3	5298.4	100.0	5300	19	Human TIGR promote
4	5298.4	100.0	5300	19	Human TIGR promote
5	5298.4	100.0	5300	19	Human TIGR promote
6	5298.4	100.0	5300	19	Human TIGR promote
7	5298.4	100.0	5300	19	Human TIGR promote
8	5275.4	99.5	6169	19	Human TIGR upstre
9	1858	35.1	2800	21	Human GLCIA gene e
10	176.4	3.3	283	15	AP2 sequence dbtd.
11	175.2	3.3	162450	21	Retinoblastoma bin
12	174.2	3.3	282	18	Consensus Alu repe

Result No.	Score	Query Match	Length	ID	Description
13	173.6	3.3	17327	14	044278
14	173.2	3.3	49999	20	223900
15	172.8	3.3	452	17	T42809
16	172.8	3.3	106746	21	A10225
17	172	3.2	2932	13	Q25388
18	172	3.2	2932	20	232161
19	172	3.2	2932	20	232162
20	172	3.2	43069	21	236335
21	171.6	3.2	10380	18	T67164
22	171.2	3.2	21721	20	X83427
23	171.2	3.2	22976	20	X83426
24	171	3.2	54548	21	245596
25	170.8	3.2	2617	21	AD3452
26	170.4	3.2	3234	16	Q92781
27	170	3.2	15056	19	V52967
28	170	3.2	15056	21	299933
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30	169	3.2	5543	18	T75284
31	168.4	3.2	11288	16	Q90512
32	168.2	3.2	3089	21	264958
33	167.4	3.2	555	20	V90098
34	167.4	3.2	41783	21	A35029
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36	167.4	3.2	141589	21	A35005
37	167.4	3.2	141589	21	A35030
38	167.4	3.2	162450	21	286967
39	166.8	3.1	7849	16	O94109
40	166.4	3.1	1601	21	A35191
41	166.4	3.1	1601	21	246814
42	166.4	3.1	1618	12	Q10207
43	166.4	3.1	1618	14	Q46958
44	166.4	3.1	1618	21	286905
45	166.4	3.1	1645	21	258659

ALIGNMENTS

RESULT 1

V51361 standard; DNA; 5299 BP.

AC V51361;

DT 27-OCT-1998 (first entry)

DE Human TIGR promoter region DNA.

KW TIGR: trabecular meshwork induced glucocorticoid response protein; human; diagnosis; glaucoma; polymorphism; steroid sensitivity; ss.

OS Homo sapiens.

XX W09832850-A1.

PN 30-JUL-1998.

PD 09-JAN-1998; 98WO-US00468.

PE 26-SEP-1997; 97US-0938669.

PR 28-JAN-1997; 97US-0791154.

XX (REGC) UNIV CALIFORNIA.

PA Chen H, Chen P, Nguyen TD, Polansky JR; WPI; 1998-427946/36.

DR Use of TIGR nucleic acid sequences - used for, e.g. developing products for diagnosis, prognosis and treatment of glaucoma

PT Claim 34; Fig 1; 105bp; English.

XX

CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter region which is used in a method for diagnosing
CC glaucoma in a patient. The method involves the detection of polymorphisms
CC whose presence is predictive of a mutation affecting TIGR response in the
CC patient and can be diagnostic of glaucoma or steroid sensitivity. Base
CC substitutions and base additions upstream of and within TIGR exons can
CC also be used to diagnose glaucoma.

XX Sequence 5299 BP: 1482 A; 1151 G; 1235 G; 1431 T; 0 other;

Query Match 100.0%; Score 5299; DB 19; Length 5299;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 3001 ataaagacccctgcagcgtctcgtgtctctgtgtgaaacacttcccggtatcttctcgtgtaggg 3060
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Db 3001 ataaagacccctgcagcgtctcgtgtctctgtgtgaaacacttcccggtatcttctcgtgtaggg 3060

OY 3061 ggaatctgagagagagagagcagagcctgagcagctgtgaagccacagggagaggtcagag 3120
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OY 3121 ggaacagagagcagagcagagagcctggtgtctccatccagttcctcactgtatcagcgtcagactc 3180
|||||
Db 3121 ggaacagagagcagagcagagagcctggtgtctccatccagttcctcactgtatcagcgtcagactc 3180
OY 3181 cagagccagagagcccaatgtcttcagagaaagctcaatgtaaacccaacagcccatcttctc 3240
|||||
Db 3181 cagagccagagagcccaatgtcttcagagaaagctcaatgtaaacccaacagcccatcttctc 3240
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OY 3301 ggtagcttctgtcgtgcatctcaaaaaactgtgcccagagcaggtgagaaatgtccagagattg 3360
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Oy	4741	agggggggaatactcgcgcgtctctaagaagaatgctcctccgcgaagcctggtlaagggtcgtc	4800
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Oy	5221	gctccccaagatatataaaacactctcgggaagcctggtgcagtcgaagcagaagccacccctc	5280
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        |||
Db      5281 cagcaccctctcagcacag 5299

RESULT      2
ID          VS1362
AC          VS1362 standard; DNA: 5300 BP.
XX          VS1362:
XX          27-OCT-1998 (first entry)
DE          Human TIGR promoter mutant TIGRmt1 DNA.
XX          TIGR: trabecular meshwork induced glucocorticoid response protein; human;
KW          diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX          Homo sapiens.
OS          Synthetic.
FH          Key
FT          mutation
FT          Location/Qualifiers
FT          4337
FT          /*tag= a
FT          /note= "wild type C is replaced by G"

WO9832850-A1.
30-JUL-1998.
09-JAN-1998; 98WO-US00468.
26-SEP-1997; 97US-0938669.
28-JAN-1997; 97US-0791154.
(PREC ) UNIV CALIFORNIA.

Chen H, Chen P, Nguyen TD, Polansky JR;
WPI: 1998-427946/36.

Use of TIGR nucleic acid sequences - used for, e.g. developing
products for diagnosis, prognosis and treatment of glaucoma

Disclosure: Fig 2: 105pp; English.

This sequence is a trabecular meshwork induced glucocorticoid response
protein (TIGR) promoter mutant, TIGRmt1, which is used in a method for
diagnosing glaucoma in a patient. The method involves the detection of
polymorphisms whose presence is predictive of a mutation affecting TIGR
response in the patient and can be diagnostic of glaucoma or steroid
sensitivity. Base substitutions and base additions upstream of and within
TIGR exons can also be used to diagnose glaucoma.

Sequence 5300 BP: 1482 A; 1151 C; 1236 G; 1431 T; 0 other;

Query Match      100.0%; Score 5298.4; DB 19; Length 5300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1 atccttgctcagcttaacctcagcgctattatgaaatgaaatgagataaccacatgtgaaag 60
        |||
Db      1 accttgctcagcttaacctcagcgctattatgaaatgaaatgagataaccacatgtgaaag 60

Oy      61 tccctaactgtagtagctccatcgcgagatgagtgtcttgagcagatgataaagaatca 120
        |||
Db      61 tccctaactgtagtagctccatcgcgagatgagtgtcttgagcagatgataaagaatca 120

Oy      121 ggaagaagaagatcacggttagccaaagtgtccaaagcgtgtctctctatattttagtga 180
        |||

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Db 121 ggaagaagagatccacgcttagccaagtgctccagcgctgctctctatttttagtga 180
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Db 241 catcaaaacagagctcaaaagaaacagaaatgagaatgggcaactgcccaagaaataatggcag 300
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RESULT 3
V51363
ID V51363 standard; DNA: 5300 BP.
XX
AC V51363;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human TIGR promoter mutant TIGRmt2 DNA.
XX
KW TIGR: trabecular meshwork induced glucocorticoid response protein; human;
XX diagnosis: glaucoma; polymorphism; steroid sensitivity; mutant; ss.
OS Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT mutation 4950
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FT /*tag" a
FI /note= "Wild-type C is replaced with T"
Pn W09832850-A1.
XX 30-JUL-1998.
XX 09-JAN-1998; 98WO-US00468.
XX 26-SEP-1997; 97US-0938669.
XX 28-JAN-1997; 97US-0791134.
XX (REGC ) UNIV CALIFORNIA.
XX
PI Chen H, Chen P, Nguyen TD, Polansky JR;
XX WPI: 1998-427946/36.
XX
PT Use of TIGR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
XX
PS Disclosure: Fig 2; 105pp; English.
XX
CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter mutant, TIGRmt2, which is used in a method for
CC diagnosing glaucoma in a patient. The method involves the detection of
CC polymorphisms whose presence is predictive of a mutation affecting TIGR
CC response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
CC TIGR exons can also be used to diagnose glaucoma.
XX
SQ Sequence 5300 BP; 1482 A; 1151 C; 1235 G; 1432 T; 0 other;
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Query Match 100.0%; Score 5298.4; DB 19; Length 5300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 4861 ggaatctcagcttccatgaacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 4920

[illegible]

CC diagnosing glaucoma in a patient The method involves the detection of
CC polymorphisms whose presence is predictive of a mutation affecting TIGR
CC response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
CC TIGR exons can also be used to diagnose glaucoma.
XX
SQ Sequence 5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 other;

Query Match	100.0%;	Score 5298.4;	DB 19;	Length 5300;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 5299;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

OY	1	attcttgccttacccttcagggcctattagaagaatgaaatgaaatataccaatcttgaaag	60
Db	1	atctttgttcgcttbaaccttcagggcctatacgaagaatgaatgaaatccaatcttgaaag	60
OY	61	tcctataaactgctatagacctcattcccttgatgactctcttgccggagatgatatgaagaaatca	120
Db	61	tcctataaactgctatagacctcattcccttgatgactctcttgccggagatgatatgaagaaatca	120
OY	121	ggaaagaagaatataccaaagttaagccaagtctgcacagctctgtctgcctctatttaatga	180
Db	121	ggaaagaagaatataccaaagttaagccaagtctgcacagctctgtctgcctctatttaatga	180
OY	181	cagatgcttgcctctgcacagaagcctattcttcagaagaaacatcacatcccaatattgtaaatc	240
Db	181	cagatgcttgcctctgcacagaagcctattcttcagaagaaacatcacatcccaatattgtaaatc	240
OY	241	catcaaacagagagctataagaaacaggaatgaaatgtggacatctgcaccaaggaaaaatgccag	300
Db	241	catcaaacagagagctataagaaacaggaatgaaatgtggacatctgcaccaaggaaaaatgtccag	300
OY	301	ggagagcaaatatagtgtgaaaaataaactcttcctctgtttctttaattccagaaaaaatg	360
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Db	541	ggcatcacctctggggaggcgaagtccaggaaggtcatgtttgccaaggaactaaacaataac	600
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Db	781	gacatggtttaaagaagccaacccaagacatgttgagccttcctcaagcagcagctgccttcagca	840
OY	841	ggagaccctgagagcatctgctcttgaggaaagccagtttctctaaggaatcttaagaatac	900
Db	841	ggagaccctgagagcatctgctcttgaggaaagccagtttctctaaggaatcttaagaatac	900

OY	901	ctgaaagatcatgaattcttaaccattttaagtataaacaatatgcyatcatatcag	960
Db	901	ctgaaagatcatgaattcttaaccattttaagtataaacaatatgcyatcatatcag	960
OY	961	cttagaagatggctcccaattttaagaagcagaacatacaaggaataagctgctccagctcc	1020
Db	961	cttagaagatggctcccaattttaagaagcagaacatacaaggaataagctgctccagctcc	1020
OY	1021	ggaataggatcagaaatcataatgaatactatgctcccaactcccaactttctcagaatgac	1080
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Db	1201	tgctcagcccactcccgctcccaacaggaagctccccaacttaagctcttcgcatcaagatgt	1260
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Db	1261	tacagccgaagatctcgttgagagggtgagagtgctgtctctacactacactatgactctac	1320
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Db	1501	agctctccataaagctcgtggaattacaggaatgatactacccgcgcgcgcgaaggtctaggtc	1560
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OY	1921	tgggtgtctctgaagaaacctcgcagaccccgctgcacactgtgttttttataactctctag	1980
Db	1921	tgggtgtctctgaagaaacctcgcagaccccgctgcacactgtgttttttataactctctag	1980
OY	1981	gaacctgtgctttcatcttctctgtgtgtgactgtgttcatctacaggaatcatcatgtgaact	2040

Dh	1961	gaccgttgctcttcattctctgtgtgacgttcgtcttcattccacaggtcattctgtacaatt	2040
Qy	2041	tattgtgacttaatatctgtccagaaacccagagagacaataatgtgtgacaaagcacgtacgc	2100
Dh	2041	tattgtgacttaatatctgtccagaaacccagagagacaataatgtgtgacaaagcacgtacgc	2100
Qy	2101	ccacacctcgtgtgaggtgtgacagttcttcattgtgaaagacgtgtgcaagaataatlaatagc	2160
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OY 5281 caggcacccttcagcacagc 5300
DB 5281 caggcacccttcagcacagc 5300

RESULT 5
V51366
ID V51366 standard; DNA: 5300 BP.
XX
AC V51366;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human TIGR promoter mutant TIGRmt5 DNA.
XX
KW TIGR: trabecular meshwork induced glucocorticoid response protein; human;
diagnosis: glaucoma; polymorphism: steroid sensitivity; mutant; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation 4262
FT /*tag= a
FT /note= "Wild-type G is replaced with A"
XX
PN MO9832850-A1.
XX
PD 30-JUL-1998.
XX
PF 09-JAN-1998; 98MO-US00468.
XX
PR 26-SEP-1997; 97US-0938659.
PR 28-JAN-1997; 97US-0791154.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Chen H, Chen P, Nguyen TD, Polansky JR.
XX
DR WPI: 1998-427946/36.
XX
PT Use of TIGR nucleic acid sequences - used for, e.g. developing
products for diagnosis, prognosis and treatment of glaucoma
XX
PS Disclosure: Fig 2: 105pp: English.
XX
CC This sequence is a trabecular meshwork induced glucocorticoid response
protein (TIGR) promoter mutant, TIGRmt5, which is used in a method for
diagnosing glaucoma in a patient. The method involves the detection of
polymorphisms whose presence is predictive of a mutation affecting TIGR
response in the patient and can be diagnostic of glaucoma or steroid
sensitivity. Base substitutions and base additions upstream of and within
TIGR exons can also be used to diagnose glaucoma.
CC
CC TIGR exons can also be used to diagnose glaucoma.
XX
SQ Sequence 5300 BP: 1483 A; 1152 C; 1234 G; 1431 T; 0 other:

Query Match 100.0%; Score 5298.4; DB 19; Length 5300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 QY 3901 taaaacaaaccccaattctgttaaatgctcccaagttcagagcttaacctgcagaaaccaatac 3960
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 Db 4441 ctttgaataattagacctctcctgtcgtgatacttctgttttaacataataataaacaatgtttaa 4500
 QY 4501 attttgatatcttgataatcatattcatattcatattctgtttcctcttgtaataataattt 4560
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 Db 4501 attttgatatcttgataatcatattcatattcatattctgtttcctcttgtaataataattt 4560
 QY 4561 atatatattgaaaaaacattctctcgtgaagaagttccccaagatttccaaatgaggtctctg 4620
 |||||||
 Db 4561 atatatattgaaaaaacattctctcgtgaagaagttccccaagatttccaaatgaggtctctg 4620
 QY 4621 catgcacaacacacagaaatgaagaactgtatttagaggtcaaacattgacattggtcctgaga 4680
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 Db 4621 catgcacaacacacagaaatgaagaactgtatttagaggtcaaacattgacattggtcctgaga 4680
 QY 4681 tgcagaagctgaataattagaagaagttctcccaagaatacacaagtttcttaagaagctgaggtctg 4740
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 Db 4681 tgcagaagctgaataattagaagaagttctcccaagaatacacaagtttcttaagaagctgaggtctg 4740
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RESULT 7
 V51364
 ID V51364 standard; DNA; 5304 BP.
 XX
 AC V51364;
 XX
 DT 27-OCT-1998 (first entry)
 DE Human TIGR promoter mutant TIGRmt3 DNA.
 XX
 KW TIGR: trabecular meshwork induced glucocorticoid response protein; human;
 XX diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT mutation 4997..5002
 FT /tag= a
 FT (note= "Wild-type TG is replaced with TGTGTG"
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 MO9832850-A1.
 XX
 PD 30-JUL-1998.
 XX
 PE 09-JAN-1998: 98MO-US00468.
 XX
 PR 26-SEP-1997: 97US-0938669.
 PR 28-JAN-1997: 97US-0791154.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Chen H, Chen P, Nguyen TD, Polansky JR.
 XX
 DR WPI: 1998-427946/36.
 XX
 PT Use of TIGR nucleic acid sequences - used for, e.g. developing
 PT products for diagnosis, prognosis and treatment of glaucoma
 XX
 PS Disclosure: Fig 2: 105pp; English.
 XX
 CC This sequence is a trabecular meshwork induced glucocorticoid response
 CC protein (TIGR) promoter mutant, TIGRmt3, which is used in a method for
 CC diagnosing glaucoma in a patient. The method involves the detection of
 CC polymorphisms whose presence is predictive of a mutation affecting TIGR

[illegible]

QY	3121	ggacaggagagcgacgagcgaaagcgcgggtgctccatccatgctccatccatgcatacgcatacgcatac	3180
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QY	3181	cagagccgagagcgacacatctctccagaaagcgcccatgaccccaacagccacatcttcc	3240
Db	3181	cagagccgagagcgacacatctctccagaaagcgcccatgaccccaacagccacatcttcc	3240
QY	3241	tcacctaaagcatagacaaatgagcatcttgccataacccaataagaaatgacagagactaaatctgt	3300
Db	3241	tcacctaaagcatagacaaatgagcatcttgccataacccaataagaaatgacagagactaaatctgt	3300
QY	3301	ggtagctctttgcccggatcttcaaaaactcgggcccagcgacagtgcgaaatctgcagagatctg	3360
Db	3301	ggtagctctttgcccggatcttcaaaaactcgggcccagcgacagtgcgaaatctgcagagatctg	3360
QY	3361	ttaaacttttcaacctctgacccagcaccocccagcgacgtccagtcagctgtcgtgacgacag	3420
Db	3361	ttaaacttttcaacctctgacccagcaccocccagcgacgtccagtcagctgtcgtgacgacag	3420
QY	3421	agtgacccctgcacgcgacaggggagagaaagaaagagagatglatgtagcaagaaag	3480
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QY	3481	acagatctatccaagggcagctgggaaattgacccaagggatctatgattccacgtgatcccg	3540
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QY	3541	gttccaaagagcgacagggctatctgttggggaaaaaatcagcttcaagggaagtctgggga	3600
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QY	3601	cctgattctcaatcctatctatcttccctcttcaacagctcgagtaactctgagcaagtccacag	3660
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QY	3661	gtagtaactgagcgtctgtaagaatctatctagttctccctcttcaaggaaacatcttctcgt	3720
Db	3661	gtagtaactgagcgtctgtaagaatctatctagttctccctcttcaaggaaacatcttctcgt	3720
QY	3721	ggagtttagccagacaaaggggcaatccggtctctcttcttaacagagaaacatcttccaaag	3780
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QY	3781	taaaagccaaagacgtcttcaagcctlaaggctctgacgtacataatgtaatcttctgaaat	3840
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QY	3841	catttcagcgatcttcactctctgcgatccagaaatgagacgtatccctcttgctcagctg	3900
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QY	3901	taaaacaaaccccaatttgtaaatgctccaagttccaggtcttaacgtccagaaacaaatcaat	3960
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QY	3961	aagaaatgaatcctttagagcaaaacgtgtcttccacaccccttgaggtgctgcgcagggc	4020
Db	3961	aagaaatgaatcctttagagcaaaacgtgtcttccacaccccttgaggtgctgcgcagggc	4020
QY	4021	agtttggaatatttacttccacaagatgacacgtgtgtgtgtatcaacaataaagt	4080
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QY	4081	tgtccaaagggcaatcatattccaagtgtcctaaagtacatctctgcacagtttctgtatct	4140
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QY	4141	ttattggttatgtgcatttgccttctgtttcttctccttgggtttatattgaatgtaaagcag	4200
Db	4141	ttattggttatgtgcatttgccttctgtttcttctccttgggtttatattgaatgtaaagcag	4200
QY	4201	ggattatataacctcaatctccaagaagccgttgtaatttgatgtaggaaataataatctt	4260

[illegible]

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RESULT	8		
ID	V51368		
AC	V51368 standard; DNA; 6169 BP.		
XX	V51368;		
DT	27-OCT-1998 (first entry)		
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DE	Human TIGR upstream region and exon 1 DNA.		
XX			
KW	TIGR; trabecular meshwork induced glucocorticoid response protein; human; diagnosis; glaucoma; polymorphism; steroid sensitivity; ss.		
OS	Homo sapiens.		
XX			
FH			
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FT		/number= 1	
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FT		/tag= b	
FT		/product= "TIGR"	
FT	Intron	/note= "partial coding sequence"	
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FT		/number= 1	
FT		/note= "partial intron sequence"	
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PN	WO9832850-A1.		
XX			
PD	30-JUL-1998.		
XX			
PE	09-JAN-1998; 98WO-US00468.		
XX			
PR	26-SEP-1997; 97US-0938669.		
PR	28-JAN-1997; 97US-0791154.		
PA	(REGC) UNIV CALIFORNIA.		
XX			
PI	Chen H, Chen P, Nguyen TD, Polansky JR;		
XX			
DR	WPI; 1998-427946/36.		
XX			
PT	Use of TIGR nucleic acid sequences - used for, e.g. developing products for diagnosis, prognosis and treatment of glaucoma		
XX			
PS	Claim 37; Fig 3; 105bp; English.		
XX			
CC	This sequence is a trabecular meshwork induced glucocorticoid response protein (TIGR) upstream region and exon 1. This DNA sequence can be used in a method for diagnosing glaucoma in a patient. The method involves the detection of polymorphisms whose presence is predictive of a mutation affecting TIGR response in the patient and can be diagnostic of glaucoma or steroid sensitivity. Base substitutions and base additions upstream of and within TIGR exons can also be used to diagnose glaucoma.		
CC			
CC			
SO	Sequence 6169 BP; 1702 A; 1389 C; 1491 G; 1587 T; 0 other;		
Query Match	99.5%; Score 5275.4; DB 19; Length 6169;		
Best Local Similarity	99.9%; Pred. No. 0;		
Matches 5298; Conservative	0; Mismatches 1; Indels 2; Gaps 2		
Oy	1 atcttgttcagtttaacctcagaagcgtatataatgaatgaaatgatatgaaccaaattgaaag 60 		
Db	1 attcttgctcagtttaacctcagaagcgtatataatgaatgatatgaaccaaattgaaag 60 		
Oy	61 tccataaaactgtatagcttcattccatcgatgagtgtctttggcagaatgataaagaatca 120 		
Db	61 tccataaaactgtatagcttcattccatcgatgagtgtctttggcagaatgataaagaatca 120 		

Oy	121	ggaagaaagagatcaccglttaagccaaagtgtccaaaggtgtgtctctcttattttatgtga	180
Db	121	ggaagaaagagatcaccglttaagccaaagtgtccaaaggtgtgtctctcttattttatgtga	180
Oy	181	cagatgtgtctctgtcacagaagctattcttcaggaacaaccatccaatgtgtaatc	240
Db	181	cagatgtgtctctgtcacagaagctattcttcaggaacaaccatccaatgtgtaatc	240
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Oy	301	gagagccaataatgatgtaaaaataaacctttcccttgtttttaatttcaggaaaaaatg	360
Db	301	gagagccaataatgatgtaaaaataaacctttcccttgtttttaatttcaggaaaaaatg	360
Oy	361	atggagaccataatcaatgtgaataaggaataacagctcagaaaaaagatgtttcccaattg	420
Db	361	atggagaccataatcaatgtgaataaggaataacagctcagaaaaaagatgtttcccaattg	420
Oy	421	taattaaagtattctgtccctggggaagagacccctcattgtagcttttgaTggaaaaatgtgaa	480
Db	421	taattaaagtattctgtccctggggaagagacccctcattgtagcttttgaTggaaaaatgtgaa	480
Oy	481	aaacgtccaaaagcattgtctgatccagatcccaaaTgtgattattttaaaaaccagat	540
Db	481	aaacgtccaaaagcattgtctgatccagatcccaaaTgtgattattttaaaaaccagat	540
Oy	541	ggcatcctctcgggggaagcgaagtctcagggaagtcagttagcaaaaggcatataaac	600
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Db	601	agcaaaatcaaaatctccgcgaatctgcaggaagaaatctggagacttcgaataac	660
Oy	661	agtgatttaggcagtttgacatgttctgcacaacctcccgctataccagggaacaaaa	720
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Db	721	attgacatgggttaagcccttgaaactttcaagggaatatgtgaataacTgaaagcaaaaa	780
Oy	781	gacatgtgttaaaagcaaccagaacatttgagccttcaaaTcagTgccccctcagca	840
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Oy	841	ggagaccctgagcattgtgccttaaggaagccagtttctttaaaggaacttaagaacctc	900
Db	841	ggagaccctgagcattgtgccttaaggaagccagtttctttaaaggaacttaagaacctc	900
Oy	901	ttgaaagttcattgaatttttaacattttaagtaataaacaatatgTgagatcataatag	960
Db	901	ttgaaagttcattgaatttttaacattttaagtaataaacaatatgTgagatcataatag	960
Oy	961	tttaagacattgtgtcccaattttataaagtcaggcatacaagataagTgtcccaagctcc	1020
Db	961	tttaagacattgtgtcccaattttataaagtcaggcatacaagataagTgtcccaagctcc	1020
Oy	1021	ggataggttcagaaatacatcttgaataacatgtgtgtcccatctcaacttttcagaatgatc	1080
Db	1021	ggataggttcagaaatacatcttgaataacatgtgtgtcccatctcaacttttcagaatgatc	1080
Oy	1081	tgtcatagcccttcacacacagggcccgatgtgtctgacctaacaacaacttcataaccga	1140
Db	1081	tgtcatagcccttcacacacagggcccgatgtgtctgacctaacaacaacttcataaccga	1140
Oy	1141	gtgcctcaaacattgtttaaaggtgtcatctcagaaggttcccatcttaaaatgtccactccc	1200
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Db	2341	gctcgtccctccgtatcgtctcgttgcatactgagctcgagatcctcttgcccaagct	2400
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Oy	2461	cccaagggaaaaggggcccccaagctccagagaaattccaaagagtggggtcagagag	2520
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Oy	2521	tgggagcggctggggcggagcgggtgcctgaaagggcagaaagctgaaagggcagag	2580
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Oy	2581	gctgcgcagatgtccagtgctgtctcaggggctgggagtttcocgtgctctctgtagc	2640
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Oy	2641	cttttatactctctcgtctggagagaaagatctatactcagagggatcagtttc	2700
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Oy	2701	ataaagctcagcgttcaaaattccaggggtggacatgggtttctctccagagagccctat	2760
Db	2701	ataaagctcagcgttcaaaattccaggggtggacatgggtttctctccagagagccctat	2760
Oy	2761	ttcaatcggagatacagaaacagagctatctccagagccgtttaattcagggaaaggtgac	2820
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Oy	2941	ggtcggcgtctgcagacggctgggcaagctgcctctccctccgggcatagctctctgcct	3000
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Oy	3001	ataaagaccctctgacgctctcgtgtctcgtgaaacacttccctgtgattctctgtagag	3060
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Oy	3661	gtatgtaacgtgagcctgtaagatactatgttcccttatagaaactcttctcgt	3720
Db	3661	gtatgtaacgtgagcctgtaagatactatgttcccttatagaaactcttctcgt	3720
Oy	3721	ggagtttagcagccaaggggaaatccggttctctttaaaggaagaaacattctctaag	3780
Db	3721	ggagtttagcagccaaggggaaatccggttctctttaaaggaagaaacattctctaag	3780
Oy	3781	taagaccaaacagattcaaacgtcagctcgtgcacatctgattgtttcttgaataat	3840
Db	3781	taagaccaaacagattcaaacgtcagctcgtgcacatctgattgtttcttgaataat	3840
Oy	3841	catttcagcagctgttaactcctgatacagaataatgagactgtaaccttgttcagctg	3900
Db	3841	catttcagcagctgttaactcctgatacagaataatgagactgtaaccttgttcagctg	3900
Oy	3901	taaaacaacacccaattgttaaatgtctcaaggttccagcttcaagcaggaacccaataat	3960
Db	3901	taaaacaacacccaattgttaaatgtctcaaggttccagcttcaagcaggaacccaataat	3960
Oy	3961	aagatatgaattctttagagcaaacctggttctccac-tctggagggtagtctccaggg	4019
Db	3961	aagatatgaattctttagagcaaacctggttctccac-tctggagggtagtctccaggg	4019
Oy	4020	cagtttggaatatcttaactcaacagatctgacacgtctgttggtatcacaacataag	4079
Db	4020	cagtttggaatatcttaactcaacagatctgacacgtctgttggtatcacaacataag	4079
Oy	4080	ttgctccaagggcaatcttatcttaagtgctctaaagttaactcttcgacgtttgtgata	4139
Db	4080	ttgctccaagggcaatcttatcttaagtgctctaaagttaactcttcgacgtttgtgata	4139
Oy	4140	tttaattgacattgccaatttgctcttgggttcttctcccttgaggttcttaatgtaagca	4199
Db	4140	tttaattgacattgccaatttgctcttgggttcttctcccttgaggttcttaatgtaagca	4199
Oy	4200	gggattttaactacgtccagaaagcctgtggaatttgatggaggaataatatact	4259
Db	4200	gggattttaactacgtccagaaagcctgtggaatttgatggaggaataatatact	4259
Oy	4260	ttggttttaacaccttcaactaaattcaacatttatccatctggagatagagcattaa	4319
Db	4260	ttggttttaacaccttcaactaaattcaacatttatccatctggagatagagcattaa	4319
Oy	4320	actcaaaagtgtgataacagatacctgtgattgttgcatctccacataagaaacaaagacat	4379
Db	4320	actcaaaagtgtgataacagatacctgtgattgttgcatctccacataagaaacaaagacat	4379
Oy	4380	tttaatactatactaatgttctgcagaatacgttgtaagtgaataatatactcaaaact	4439
Db	4380	tttaatactatactaatgttctgcagaatacgttgtaagtgaataatatactcaaaact	4439
Oy	4440	acttgaaatagaactcctcgtcgtgacatcgtgttataacataatacaaaacatgtctaa	4499
Db	4440	acttgaaatagaactcctcgtcgtgacatcgtgttataacataatacaaaacatgtctaa	4499

[illegible]

PN MO995177-A2.
XX
PD 14-OCT-1999.
XX
PF 07-APR-1999; 99MO-USO7671.
XX
PR 07-APR-1998; 98US-0056285.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Stone EM, Sheffield VC, Alward WLM, Fingert J;
DR MPI; 2000-022956/02.
XX
PT Determination of a predisposition to glaucoma by analysing mutations in
XX the GLCIA gene -
XX
PS Disclosure; Fig 1A; 137pp; English.
XX
CC The invention relates to a method for the determination of a
CC predisposition to glaucoma. The method comprises amplifying a GLCIA gene
CC with a primer pair selected from the sequences shown in 237981-238008.
CC The primers are used to determine whether a subject has or has the
CC potential to develop primary open wide angle glaucoma. The present
CC sequence represents the human GLCIA gene exon 1 and flanking sequences.
XX
SQ Sequence 2800 BP; 781 A; 588 C; 673 G; 758 T; 0 other:

Query Match	35.1%	Score	1858:	DB 21:	Length	2800:
Best Local Similarity	99.9%	Pred	No. 0:			
Matches 1869:	Conservative	0:	Mismatches	0:	Indels	1:
						Gaps
OY	3431	agcgacagggagagagagaaaaagagagagatgatactgagccaagaaagacagattcat	3490			
Db	1	agcgacagggagagagaaag-aaaagagaggatgagtatgagcaagaaagacagattcat	59			
OY	3491	tcaagggcgagtgvggaattgacacacaggggattatgaatcccgctacccgtggtcttcaggg	3550			
Db	60	tcaagggcgagtgvggaattgacacacaggggattatgaatcccgctacccgtggtcttcaggg	119			
OY	3551	gcagggcctatctgtggtgggggaaaaatcaggttcacaagggaaatcgaggagacctgtattct	3610			
Db	120	gcagggcctatctgtggtgggggaaaaatcaggttcacaagggaaatcgaggagacctgtattct	179			
OY	3611	aatactataattttcccttaccagagctgagtaattctctgagcaagtcacaaggtagtaactg	3670			
Db	180	aatactataattttcccttaccagagctgagtaattctctgagcaagtcacaaggtagtaactg	239			
OY	3671	aggcgctgaagtattattggtttctcccttatatggagaccttttctctgttgagttagga	3730			
Db	240	aggcgctgaagtattattggtttctcccttatatggagaccttttctctgttgagttagga	299			
OY	3731	gcacaaagggcgaatcccggttcttcttcaacagagaaagaaacatctcctaagagtagtaagccaaa	3790			
Db	300	gcacaaagggcgaatcccggttcttcttcaacagagagaaacatctcctaagagtagtaagccaaa	359			
OY	3791	cagattcaagccctaggtctctgcgactataatgattggttttttgaaaaatcatcttcagcg	3850			
Db	360	cagattcaagccctaggtctctgcgactataatgattggttttttgaaaaatcatcttcagcg	419			
OY	3851	atgtttactatctgtgttcagaaaaagaaactgtaaccccttctgtcagctgtataacaaaa	3910			
Db	420	atgtttactatctgtgttcagaaaaagaaactgtaaccccttctgtcagctgtataacaaaa	479			
OY	3911	cccatcttgtaaatgctcgaagttcagagcttaactgcagaaaccaatcaaatagaaatagaa	3970			
Db	480	cccatcttgtaaatgctcgaagttcagagcttaactgcagaaaccaatcaaatagaaatagaa	539			
OY	3971	tctttaagagcaaacgtgttcttccactctgtgaagttgagctcggccaagggcagattggaaa	4030			
Db	540	tctttaagagcaaacgtgttcttccactctgtgaagttgagctcggccaagggcagattggaaa	599			

OY 1401 CG-----caagcccgccgaattttttatgtatgtagtagaataagggtttacccat 1452
 Db 156 CCGCGCGCCACCGCCCGCGCTAATTTTGTATTTTAGTAGACACGGGGTTTACCACTGT 97
 OY 1453 tagccgcagctggctctgaacctcctgaacctgaagtgatccaccacacctcaagcctctaag 1512
 Db 96 TCGCCAGCGCTGGCTTGTAACCTCTGACCTCAGCTCAGTGTGATCCACCCACCGCTGCCAAG 37
 OY 1513 tgcctggattacagcatgaatcagtcacgcgcgcgcgc 1548
 Db 36 TCGTGGATTACAGGTGTGAGCCACCGCCAGCC 1
 RESULT 11
 ID 286967/c
 XX 286967 standard; DNA: 162450 BP.
 AC 286967;
 XX
 DT 16-MAY-2000 (first entry)
 XX
 DE Retinoblastoma binding protein-7 genomic DNA sequence.
 KW RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation;
 KW diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;
 KW benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukemia;
 KW lymphoma; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200000607-A1.
 PD 06-JAN-2000.
 XX
 PF 30-JUN-1999; 99WO-1B01242.
 XX
 PR 30-JUN-1998; 98US-0091315.
 PR 10-DEC-1998; 98US-0111909.
 XX
 PA (GEST) GENSET.
 PI Bougueleret L;
 DR WPI: 2000-117170/10.
 XX
 PT Novel nucleic acid and polymorphic markers used for diagnosis of
 PT diseases, especially those involving abnormal cell proliferation and
 PT differentiation -
 XX
 PS Claim 1; Page 118-163; 223pp; English.
 XX
 This sequence represents the retinoblastoma binding protein-7 (RBP-7)
 genomic sequence of the invention. The RBP-7 coding sequence and
 regulatory sequences are useful for the recombinant production of the
 protein and for expressing heterologous nucleic acids. Primers and probes
 derived from the RBP-7 nucleotide sequence (e.g. 287035-287099) are
 useful for DNA amplification and detection methods. RBP-7 biallelic
 markers (see 286963-287034) are useful for diagnosis of disease related
 to alteration in the regulation or in the coding regions of the RBP-7
 gene and for prognosis/diagnosis of an eventual treatment with
 therapeutic agents, especially agents acting on pathologies involving
 abnormal cell proliferation and/or differentiation, these include
 thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers,
 including breast cancer, sarcoma and other neoplasms, bladder cancer,
 colon cancer, lung cancer, prostate cancer, various leukaemias, and
 lymphomas. RBP-7 antibodies are useful as diagnostic agents.
 XX
 Sequence 162450 BP; 45465 A; 30661 C; 32637 G; 53673 T; 14 other:

QY	1280	agggtgaagagctctgtgtcttaccactccctgtatagctctaccactgagctcatgtgaac	1339
Db	141925	AGAGTCTGCTCTGTGTGCCAGGCTGGAGTGCCTGGCAGATCTCAATTCTACCTACACCC	141866
QY	1340	tctgtctcccaaggttcaagaacatctctcttctctcaagctccgcgctgtagctggactaacg	1399
Db	141865	TCCACCTCCCGGGTTCAAGGCATATCTCCTGCTGCGGCTCCCAATAGCGGGACTACAG	141806
QY	1400	ggcagcgcgcgcgctaattttgtatctgtttagtagagtaggggttttaacatatagcccg	1459
Db	141805	GCACACGCCAAGCTAATTTTGTATTTTTCACAGATGGGGTTTCACTCATTTGGTCA	141746
QY	1460	gctgtctctgaactctctgacctcaggtatcatcaaccacccctcaagcctctaaagtgtcgg	1519
Db	141745	GCTGTCTCAAACTCCTGACCTCAGATGATCCACCTCTCGGCGCTCCCAAAATGCTGG	141686
QY	1520	attacagcatgatgtacacgcggcccgcg	1547
Db	141685	ATTACAGGTGTGAGCCACTGTGTCCAC	141658

RESULT	12	
TT62346/C		
ID	TT62346	standard; DNA; 282 BP.
XX		
AC	TT62346;	
XX		
DT	11-JUN-1997	(first entry)
XX		
DE	Consensus Alu repeat sequence.	
XX		
KW	Bubble: interspersed repetitive element; ligation; annealing; primer;	
KW	PCR; polymerase chain reaction; amplification; chromosomal aberration;	
KW	genetic disorder; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	primer_bind	22..45
FT		/*tag= a
FT		/note= "binds primer 47-23 (TT62347)"
FT	primer_bind	216..236
FT		/*tag= b
FT		/note= "binds either primer Alu-S (TT62348) or
FT		Alu-J (TT62349)"
FT	primer_bind	263..282
FT		/*tag= C
FT		/note= "binds primer Alu-end (TT62350)"
XX		
PN	US5597694-A.	
XX		
PD	28-JAN-1997.	
XX		
PF	07-OCT-1993;	93US-0133629.
XX		
PR	07-OCT-1993;	93US-0133629.
XX		
PA	(MASI) MASSACHUSETTS INST TECHNOLOGY.	
PI	Housman DE, Munroe DJ;	
XX		
DR	WPI; 1997-108321/10.	
XX		
PT	Amplification of nucleic acid having interspersed repetitive element	
PT	- using bubble oligo:nucleotide	
XX		
PS	Disclosure; Column 19-20; 16pp; English.	
XX		
CC	The invention relates to the amplification of region of DNA containing	
CC	interspersed repetitive elements (IRE) such as the Alu repeat sequence	
CC	presented here. The method involves ligating a double stranded DNA	
CC	structure with a non-complementary region, a 'bubble', in the	

CC amplified by the primer pair R14B264/O560mak (T42806-7). The primers
CC also simultaneously amplify the loci Q900 (T42808) and Q120 (T42810).
CC The primers can be used for gene mapping, to assess paternity, maternity
CC and identity of children or in forensic science. In particular, they can
CC be used for the DNA fingerprinting identification of genetically related
CC or unrelated individuals.

XX
SQ Sequence 452 BP; 149 A; 92 C; 106 G; 85 T; 20 other;

Query Match 3.3%; Score 172.8; DB 17; Length 452;

Best Local Similarity 86.4%; Pred. No. 1.2e-30;

Matches 204; Conservative 1; Mismatches 23; Indels 8; Gaps 1;

Qy 1321 acctgagctactgcaacctctgctccaggttcaagcaattcctctgctcagcctcc 1380
Db 312 attctagctactgcaacctctgctccaggttcaagcaattcctctgctcagcctcc 253
Qy 1381 cgcgtagctggaactacagcg-----cagcccgctaatcttctgtagtagta 1432
Db 252 cgartagctgggattacagctgctccaggttcaagcaattcctctgctcagcctcc 193
Qy 1433 gagaatggggttcaacataltagccggctgctctgaactcctgacctcaggtgatcca 1492
Db 192 gagacgggggttccacacgttgccaggtgctctcaaaactcctgacctcaggtgatctg 133
Qy 1493 cccacctcagctcctcaaatgtctggaattacaggaatgagtcacccggccggcc 1548
Db 132 cccgctcagctcctcaaatgtctggaattacaggaatgagtcacccggccggcc 77

Search completed: December 3, 2000, 19:16:21
Job time: 42641 sec

